

FIG. 1

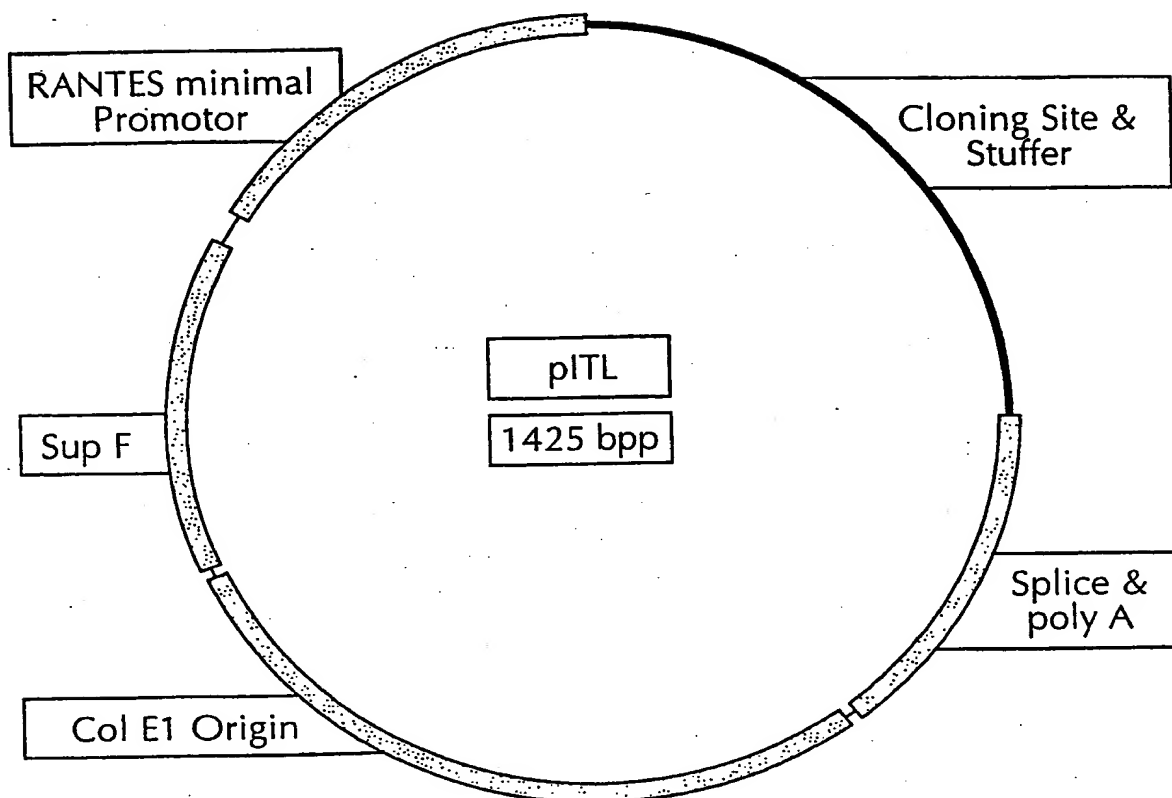


FIG. 2

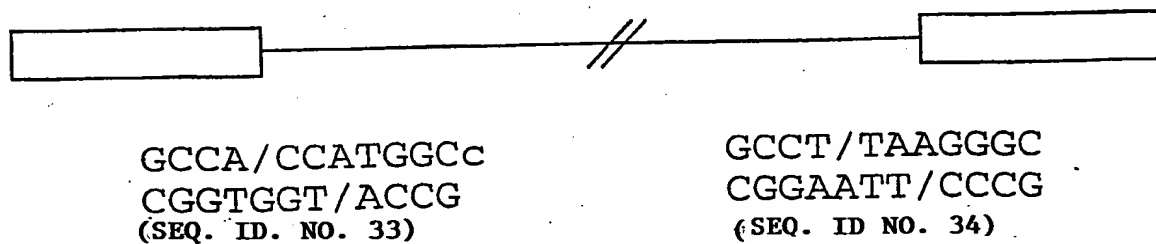




FIG. 3A

60  
MRPSGTAGALLALLAALCPASRALEKKVCQGTSNKLTQLTGFEDHFLSLQRMFNCEVVLGNLEITYVQRNYD  
M---ELAAALCRWGLLLALLP-PGA-AST-VCTGTDMLKRLPASPEHLDMLRHLVQGCQVVOGNLELTYLPTNAS  
57

125  
LSFLKTIQEVAGYVLIANTVERIPILENLQIRGNMYENSYALAVLSNYD--AN---KT-----GLKELPMRNL  
140  
LSFLQDIEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL  
122  
147

175  
\* \* \* \* \*  
QEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHSGCQKCDPSCPNGS-CWGAGEENCQKLTKII  
TEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTIDTNRSRACHPCSPMCK-GSRCWGESSEDCQSLTRTV  
175

289  
\* \* \* \* \*  
CAQQCSGRGKSPSDCCCHNOCAAGCTGPRSDCLVCRKFRDEATCKDTPPLMLYNPTTYQMDVNPEGKYSFGA  
CAGGCA-RCKGPLPTDCCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGA  
295

350 \*  
\* \* \* \* \*  
YVVTDHGSCVRACGADSYEME-EDGVRKCKKCEGPCRKVCNCGIGIGEFKDSLSINATNIKHFKNCTSIGDHLIL  
YLSTDVGSCTLVCPLHNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFL  
352

438  
PVAFRGDSFTHTPPLDPQELDKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQPGQFSLAVVSLNITS  
PESFDGDPASNTAPLQPEQLQVFFETLEEITGYLYISAWPDSLPLDSVFQNLQVIRGRILHNGAYSLTLQGLGISW  
445

## REPLACEMENT SHEET



FIG. 3C

929

THQSDVWSYGVTVWELMTFGSKPYDGI PASEISSILEKGERLPQPPICTIDVYIMVVKCWMIDADSRPKFRELII  
THQSDVWSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVVKCWMIDSECRPRFRELVS  
940

EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGFF  
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGFF  
1010  
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGFF  
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGFF  
1040

SSPSTSRTPLLSSLATSNNSTVACIDRN--GLQSCPIKEDSFLQRYSSDPTGAL-T  
RSSSTRSGGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMGAAGLQSLPTHDPSPLOQRYSEDPTVPLPS  
1137

E-D--SIDDTFLPVPEYINQ-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNVTQVTCVNS  
ETDGYVAPLTCSPQPEYVNPQDVRPQPPSPREGPLPAARPAGATLERPKTLPKGKNGVVKDVFAFGGAVENPEYL  
1120

TFDSTFLPVPEYINQ-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNVTQVTCVNSTFDSP  
TPQGTCSPOPEYVNPQDVRPQPPSPREGPLPAARPAGATLERPKTLPKGKNGVVKDVFAFGGAVENPEYLTPQGG  
1300

AHWAQKGSHQ-ISL--DNPDYQ-QDFFPKEAKPNGIFKGST--AENAEYLR-VAPQSSEFIGA (SEQ. ID NO. 35)  
AAP-QPHPPPAFSPAFDNLYYWDQDPPERGAPPS-TFKG-TPTAENPEYLGLDVPV (SEQ. ID NO. 36)  
1255



FIG. 4A

57  
MELAAALCRWGLLLALLPPGAASQVCTGTCTDMKRLRPASPETHLDMLRHLVQGCQVQGNLELTYLPTNASLS  
MIIMELAAWCRWGFLALLPPGIAGTQVCTGTCTDMKRLRPASPETHLDMLRHLVQGCQVQGNLELTYVPANASLS  
60

117  
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT  
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT  
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT  
120

176  
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA  
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA  
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA  
180

236  
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTTFGASCV  
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTTFGASCV  
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTTFGASCV  
240

356  
TACPYNLSTDVGSC TLVCPPLHNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF  
TACPYNLSTDVGSC TLVCPPLHNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF  
TACPYNLSTDVGSC TLVCPPLHNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF  
360

416  
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLRLDLSVFQNLQVIRGRILHNGAYSLTLQ  
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLRLDLSVFQNLQVIRGRILHNGAYSLTLQ  
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLRLDLSVFQNLQVIRGRILHNGAYSLTLQ  
420





FIG. 4C

SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPICITIDVYIMVVKCWMIDSECRP 950  
SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPICITIDVYIMVVKCWMIDSECRP 955

RFRELVSFSEFMRMARDPQRFVVIQNEIDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPOQFFCPDPAPGAGGM 1010  
RFRELVSFSEFMRMARDPQRFVVIQNEIDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPOQFFCPDPAPGAGGM 1015

VHRRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMGAAGLQSLPHTDPSPLQRYSEDPT 1070  
VHRRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMGAAGLQSLPHTDPSPLQRYSEDPT 1075

VPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTILSPGKNGVVKDVFAFGGAVE 1130  
VPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTILSPGKNGVVKDVFAFGGAVE 1193  
LPLPPETDGYVAPLACSPQPEYVNQSEVQPPPLTPEGPLPPVRPAGATLERPKTILSPGKNGVVKDVFAFGGAVE 1135  
LPLPPETDGYVAPLACSPQPEYVNQSEVQPPPLTPEGPLPPVRPAGATLERPKTILSPGKNGVVKDVFAFGGAVE 1198

NPEYLTPOGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1255 (SEQ. ID NO. 36)  
NPEYLTPOGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV 1263 (SEQ. ID NO. 37)